

AATTCGTTCT ACCTTCTCTG AACCCAGTG GTGTGTCAAG GCCGGACTGG GAGCTTGGGG 60  
 GAAGAGGAAG AGGAAGAGGA ATCTGCGGCT CATCCAGGGA TCAGGGTCCT TCCCAAGTGG 120  
 CCACTCAGAG GGGACTCAGA GCAAGTCTAG ATTTGTGTGG CAGAGAGAGA CAGCTCTCGT 180  
 TTGGCCTTGG GGAGGCACAA GTCTGTTGAT AACCTGAAGA CA 222  
 ATG GAT GTC GAT GAG GGT CAA GAC ATG TCC CAA GTT TCA GGA AAG GAG 270  
 Met Asp Val Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu  
 1 5 10 15  
 AGC CCC CCA GTC AGT GAC ACT CCA GAT GAA GGG GAT GAG CCC ATG CCT 318  
 Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro  
 20 25 30  
 GTC CCT GAG GAC CTG TCC ACT ACC TCT GGA GCA CAG CAG AAC TCC AAG 366  
 Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys  
 35 40 45  
 AGT GAT CGA GGC ATG GGT GAA CGG CCT TTC CAG TGC AAC CAG TCT GGG 414  
 Ser Asp Arg Gly Met Gly Gln Arg Pro Phe Gln Cys Asn Gln Ser Gly  
 50 55 60  
 GCC TCC TTT ACC CAG AAA GGC AAC CTC CTG CGG CAC ATC AAG CTG CAC 462  
 Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys Leu His  
 65 70 75 80  
 TCG GGT GAG AAG CCC TTC AAA TGC CAT CTT TGC AAC TAT GCC TGC CGC 510  
 Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg  
 85 90 95  
 CGG AGG GAC GCC CTC ACC GGC CAC CTG AGG ACG CAC TCC GTT GGT AAG 558  
 Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val Gly Lys  
 100 105 110  
 CCT CAC AAA TGT GGA TAT TGT GGC CGG AGC TAT AAA CAG CGA AGC TCT 606  
 Pro His Lys Cys Gly Tyr Cys Gly Arg Ser Tyr Lys Gln Arg Ser Ser  
 115 120 125  
 TTA GAG GAG CAT AAA GAG CGA TGC CAC AAC TAC TTG GAA AGC ATG GGC 654  
 Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Glu Ser Met Gly  
 130 135 140  
 CTT CCG GGC GTG TGC CCA GTC ATT AAG GAA GAA ACT AAC CAC AAC GAG 702  
 Leu Pro Gly Val Cys Pro Val Ile Lys Glu Glu Thr Asn His Asn Glu  
 145 150 155 160  
 ATG GCA GAA GAC CTG TGC AAG ATA GGA GCA GAG AGG TCC CTT GTC CTG 750  
 Met Ala Glu Asp Leu Cys Lys Ile Gly Ala Glu Arg Ser Leu Val Leu  
 165 170 175  
 GAC AGG CTG GCA AGC AAT GTC GCC AAA CGT AAG AGC TCT ATG CCT CAG 798  
 Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met Pro Gln  
 180 185 190

FIG. 1A

AAA TTT CTT GGA GAC AAG TGC CTG TCA GAC ATG CCC TAT GAC AGT GCC 846  
Lys Phe Leu Gly Asp Lys Cys Leu Ser Asp Met Pro Tyr Asp Ser Ala  
195 200 205

AAC TAT GAG AAG GAG GAT ATG ATG ACA TCC CAC GTG ATG GAC CAG GCC 894  
Asn Tyr Glu Lys Glu Asp Met Met Thr Ser His Val Met Asp Gln Ala  
210 215 220

ATC AAC AAT GCC ATC AAC TAC CTG GGG GCT GAG TCC CTG CGC CCA TTG 942  
Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg Pro Leu  
225 230 235 240

GTG CAG ACA CCC CCC GGT AGC TCC GAG GTG GTG CCA GTC ATC AGC TCC 990  
Val Gln Thr Pro Pro Gly Ser Ser Glu Val Val Pro Val Ile Ser Ser  
245 250 255

ATG TAC CAG CTG CAC AAG CCC CCC TCA GAT GGC CCC CCA CGG TCC AAC 1038  
Met Tyr Gln Leu His Lys Pro Pro Ser Asp Gly Pro Pro Arg Ser Asn  
260 265 270

CAT TCA GCA CAG GAC GCC GTG GAT AAC TTG CTG CTG CTG TCC AAG GCC 1086  
His Ser Ala Gln Asp Ala Val Asp Asn Leu Leu Leu Leu Ser Lys Ala  
275 280 285

AAG TCT GTG TCA TCG GAG CGA GAG GCC TCC CCG AGC AAC AGC TGC CAA 1134  
Lys Ser Val Ser Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser Cys Gln  
290 295 300

GAC TCC ACA GAT ACA GAG AGC AAC GCG GAG GAA CAG CGC AGC GGC CTT 1182  
Asp Ser Thr Asp Thr Glu Ser Asn Ala Glu Glu Gln Arg Ser Gly Leu  
305 310 315 320

ATC TAC CTA ACC AAC CAC ATC AAC CCG CAT GCA CGC AAT GGG CTG GCT 1230  
Ile Tyr Leu Thr Asn His Ile Asn Pro His Ala Arg Asn Gly Leu Ala  
325 330 335

CTC AAG GAG GAG CAG CGC GCC TAC GAG GTG CTG AGG GCG GCC TCA GAG 1278  
Leu Lys Glu Glu Gln Arg Ala Tyr Glu Val Leu Arg Ala Ala Ser Glu  
340 345 350

AAC TCG CAG GAT GCC TTC CGT GTG GTC AGC ACG AGT GGC GAG CAG CTG 1326  
Asn Ser Gln Asp Ala Phe Arg Val Val Ser Thr Ser Gly Glu Gln Leu  
355 360 365

AAG GTG TAC AAG TGC GAA CAC TGC CGC GTG CTC TTC CTG GAT CAC GTC 1374  
Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His Val  
370 375 380

ATG TAT ACC ATT CAC ATG GGC TGC CAT GGC TGC CAT GGC TTT CGG GAT 1422  
Met Tyr Thr Ile His Met Gly Cys His Gly Cys His Gly Phe Arg Asp  
385 390 395 400

CCC TTT GAG TGT AAC ATG TGT GGT TAT CAC AGC CAG GAC AGG TAC GAG 1470  
Pro Phe Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu  
405 410 415

FIG. 1B

TTC TCA TCC CAT ATC ACG CGG GGG GAG CAT CGT TAC CAC CTG AGC	1515
Phe Ser Ser His Ile Thr Arg Gly Glu His Arg Tyr His Leu Ser	
420 425 430	
TAAACCCAGC CAGGCCCCAC TGAAGCACAA AGATAGCTGG TTATGCCTCC TTCCCGGCAG	1575
CTGGACCCAC AGCGGACAAT GTGGGAGTGG ATTTGCAGGC AGCATTGTGT CTTTTATGTT	1635
GGTTGTTTGG CGTTTCATTT GCGTTGGAAG ATAAGTTTTT AATGTTAGTG ACAGGATTGC	1695
ATTGCATCAG CAACATTCAC AACATCCATC CTTCTAGCCA GTTTTGTTCA CTGGTAGCTG	1755
AGGTTTCCCG GATATGTGGC TTCCTAACAC TCT	1788

(SEQ.ID.NO:1)

FIG. 1C

1515-1788



GCC ACG TAC GAG AAG GAG AAC GAA ATG ATG AAG TCC CAC GTG ATG GAC	768
Ala Thr Tyr Glu Lys Glu Asn Glu Met Met Lys Ser His Val Met Asp	
245 250 255	
CAA GCC ATC AAC AAC GCC ATC AAC TAC CTG GGG GCC GAG TCC CTG CGC	816
Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg	
260 265 270	
CCG CTG GTG CAG ACG CCC CCG GGC GGT TCC GAG GTG GTC CCG GTC ATC	864
Pro Leu Val Gln Thr Pro Pro Gly Gly Ser Glu Val Val Pro Val Ile	
275 280 285	
AGC CCG ATG TAC CAG CTG CAC AGG CGC TCG GAG GGC ACC CCG CGC TCC	912
Ser Pro Met Tyr Gln Leu His Arg Arg Ser Glu Gly Thr Pro Arg Ser	
290 295 300	
AAC CAC TCG GCC CAG GAC AGC GCC GTG GAG TAC CTG CTG CTG CTC TCC	960
Asn His Ser Ala Gln Asp Ser Ala Val Glu Tyr Leu Leu Leu Leu Ser	
305 310 315 320	
AAG GCC AAG TTG GTG CCC TCG GAG CGC GAG GCG TCC CCG AGC AAC AGC	1008
Lys Ala Lys Leu Val Pro Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser	
325 330 335	
TGC CAA GAC TCC ACG GAC ACC GAG AGC AAC AAC GAG GAG CAG CGC AGC	1056
Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Asn Glu Glu Gln Arg Ser	
340 345 350	
GGT CTT ATC TAC CTG ACC AAC CAC ATC GCC CGA CGC GCG CAA CGC GTG	1104
Gly Leu Ile Tyr Leu Thr Asn His Ile Ala Arg Arg Ala Gln Arg Val	
355 360 365	
TCG CTC AAG GAG GAG CAC CGC GCC TAC GAC CTG CTG CGC GCC GCC TCC	1152
Ser Leu Lys Glu Glu His Arg Ala Tyr Asp Leu Leu Arg Ala Ala Ser	
370 375 380	
GAG AAC TCG CAG GAC GCG CTC CGC GTG GTC AGC ACC AGC GGG GAG CAG	1200
Glu Asn Ser Gln Asp Ala Leu Arg Val Val Ser Thr Ser Gly Glu Gln	
385 390 395 400	
ATG AAG GTG TAC AAG TGC GAA CAC TGC CGG GTG CTC TTC CTG GAT CAC	1248
Met Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His	
405 410 415	
GTC ATG TAC ACC ATC CAC ATG GGC TGC CAC GGC TTC CGT GAT CCT TTT	1296
Val Met Tyr Thr Ile His Met Gly Cys His Gly Phe Arg Asp Pro Phe	
420 425 430	
GAG TGC AAC ATG TGC GGC TAC CAC AGC CAG GAC CGG TAC GAG TTC TCG	1344
Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser	
435 440 445	
TCG CAC ATA ACG CGA GGG GAG CAC CGC TTC CAC ATG AGC TAA	1386
Ser His Ile Thr Arg Gly Glu His Arg Phe His Met Ser	
450 455 460	

(SEQ.ID.NO:2)

FIG. 2B

↓ Ex1/2 MDVDEGQDMS QVSGKESPPV SDTPDEGDEP MPVPEDLSTT SGAQQNSKSD RGMASNVKVE ↓ Ex3  
 TQSDENGR F1 CEMNGEECAE DLRMLDASGE KMNGSHRDQG SSALSGVGGI RLPNGKLKCD  
 ICGIVCIGPN VLMVHKRSHT F2 GERPFQCNQC GASFTOKGNL LRHIKLHSGE KPFKCHLCNY ↓ Ex6  
 F3 ACRRRDALTG HLRTHSVGKP F4 HKCGYCGRSY KORSSLEEKK ERCHNYLESM GLPGLMYPVIK ↓ Ex7  
 EETNHNEMAE DLCKIGAERS LVLDRLASNV AKRKSSMPQK FLGDKCLSDM PYDSANYEKE  
 DMMTSHVMDQ AINNAINYLG AESLRPLVQT PPGSSEVVPV ISSMYQLHKP PSDGPPRSNH  
 SAQDAVDNLL LLSKAKSVSS EREASPSNSC QDSTDTESNA EEQSGLIYL TNHINPHARN  
 GLALKEEQRA YEVLRAASEN SQDAFRVVST SGEQLKVYKC EHCRLFLDH VMYTIHMGCH F5  
 GCHGFRDPFE F6 CNMCGYHSOD RYEFSSHITR GEHRYHLS (SEQ ID NO:4)

FIG. 3

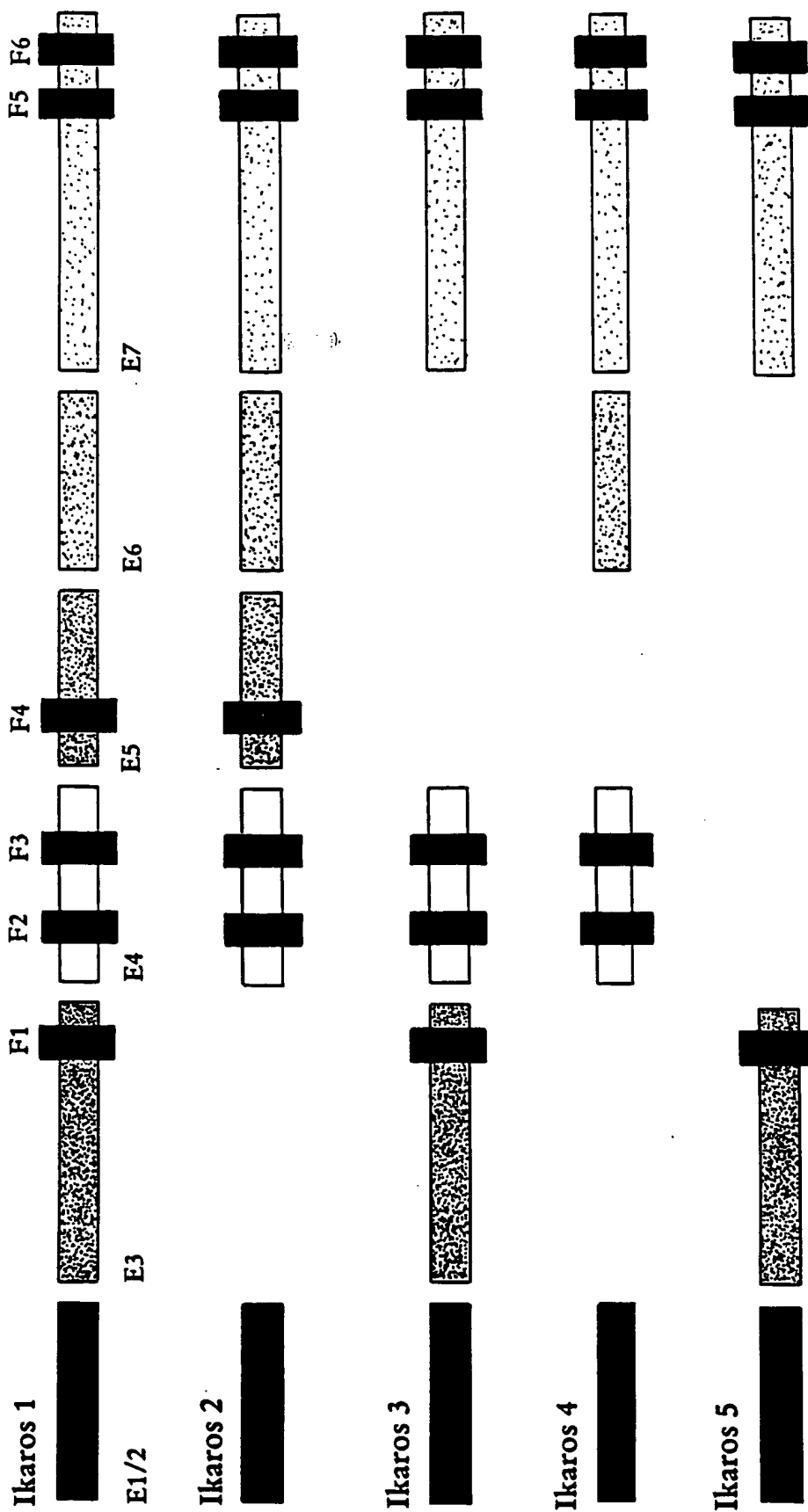
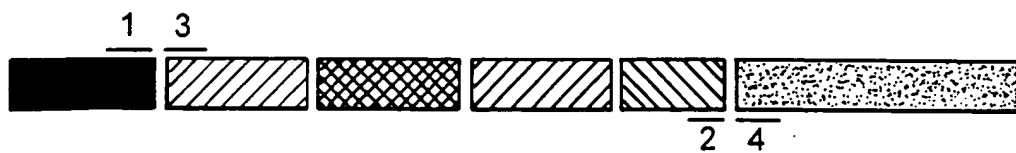


FIG. 4



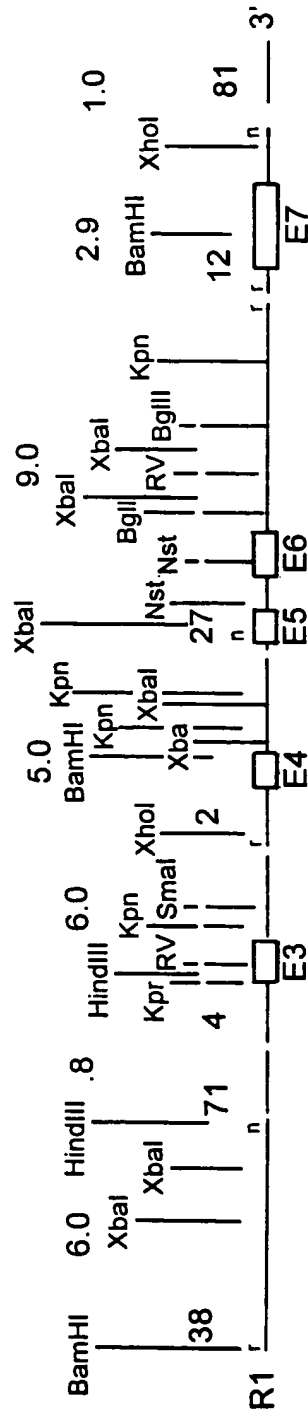
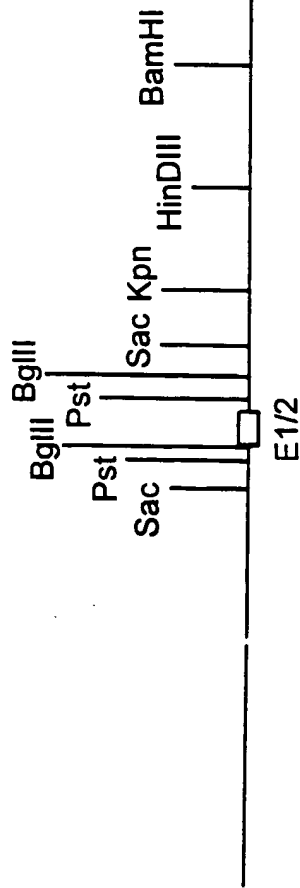
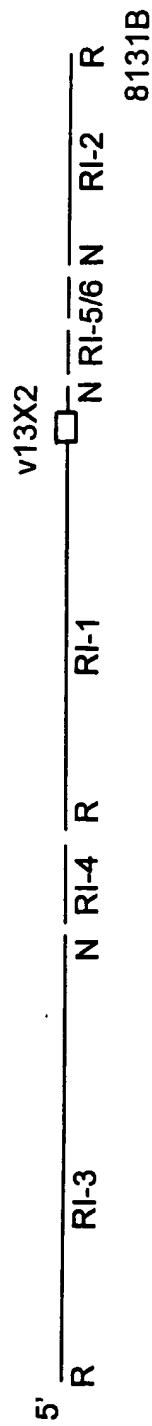
Oligo1/2 IK-1/IK-2/IK-4

Oligo3/4 IK-1/IK-3/IK-5

FIG. 5

FIG. 5





2kb

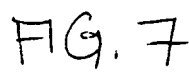
f2

f10

f4

f8

FIG. 6

[illegible]

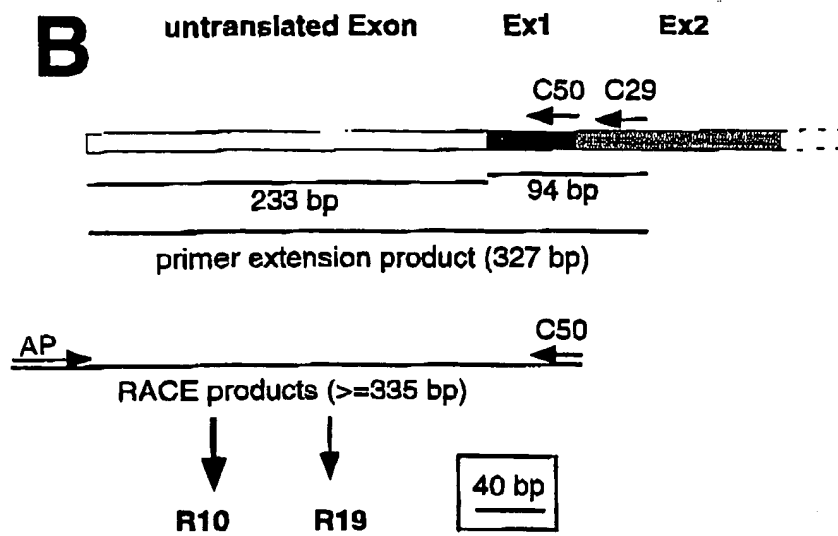
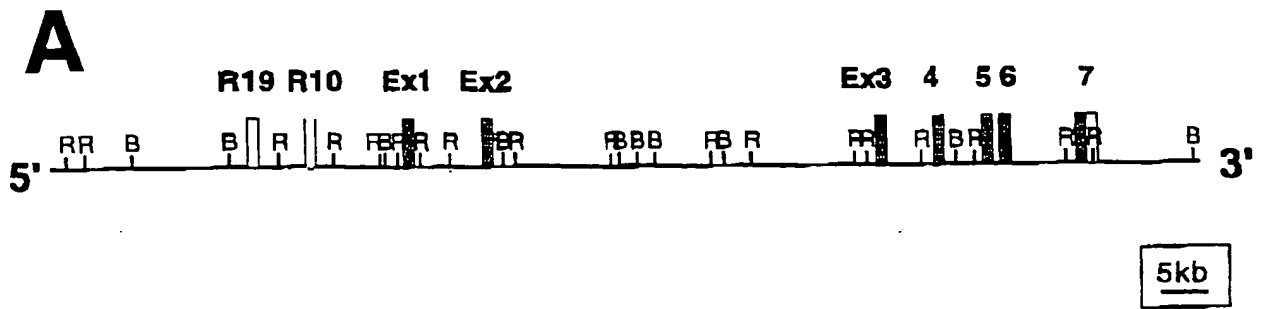


FIG. 8

**A**

Genetic map of the human HLA-B\*07:02 gene region. The map shows the arrangement of exons (α, β, γ, δ, ε, ζ, η, θ) and introns (1, 2, 3) across the 5' to 3' direction. A scale bar indicates 5kb. A legend identifies symbols for Transcription Start (TS), Transcription (T), and Splicing (S).

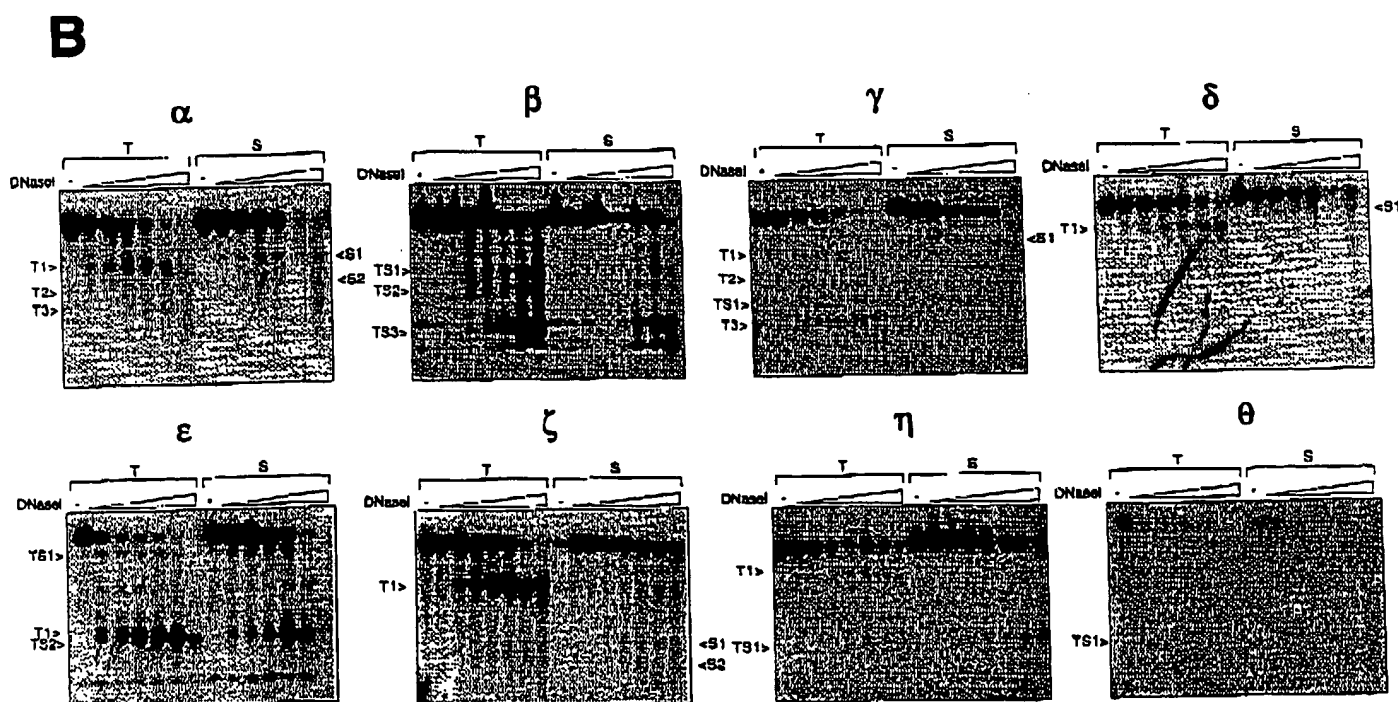


FIG. 9

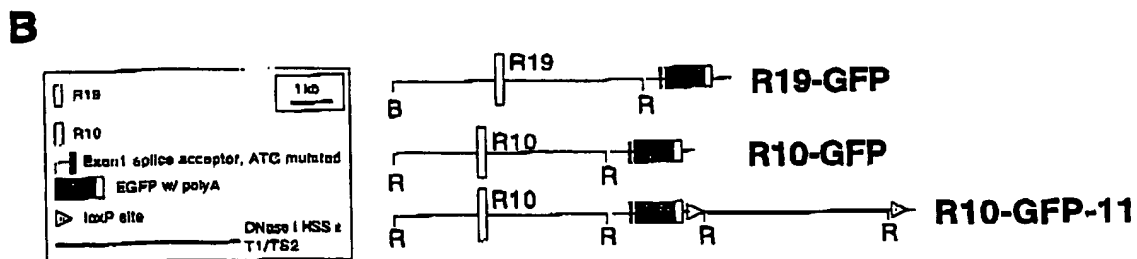
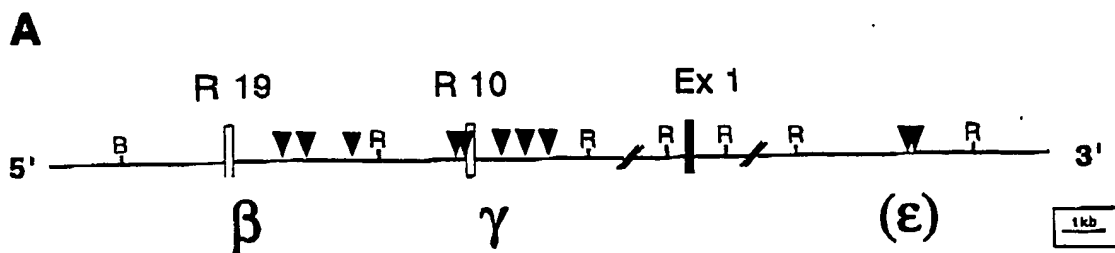
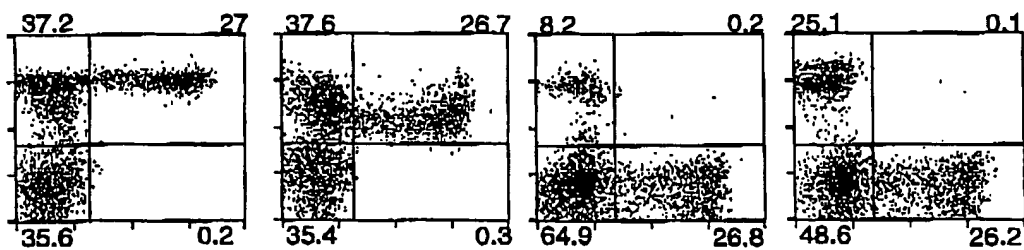


FIG. 10

# Bone Marrow

## R19-GFP<sup>F</sup>



## R10-GFP<sup>C</sup>

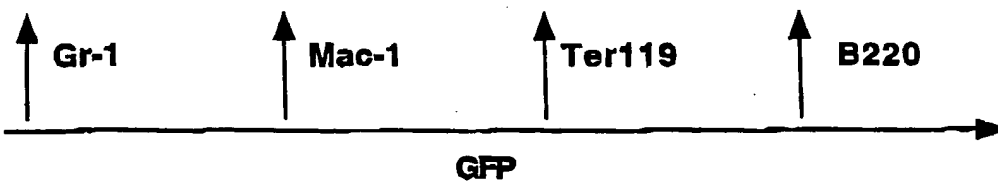
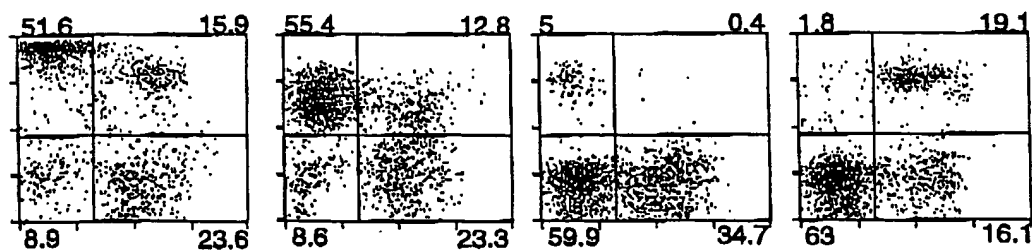
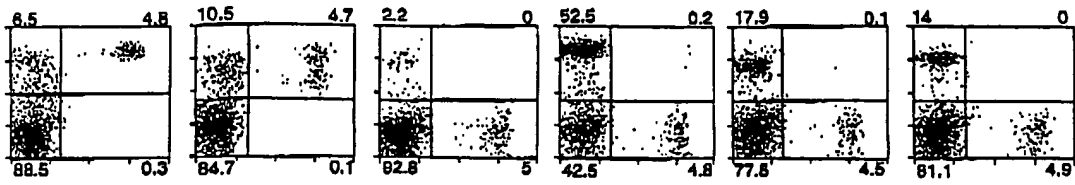


FIG. 11

# Spleen

## R19-GFP



## R10-GFP

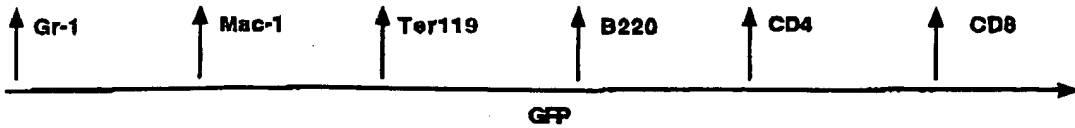


FIG. 12

CD4<sup>+</sup> / CD8<sup>+</sup> DN

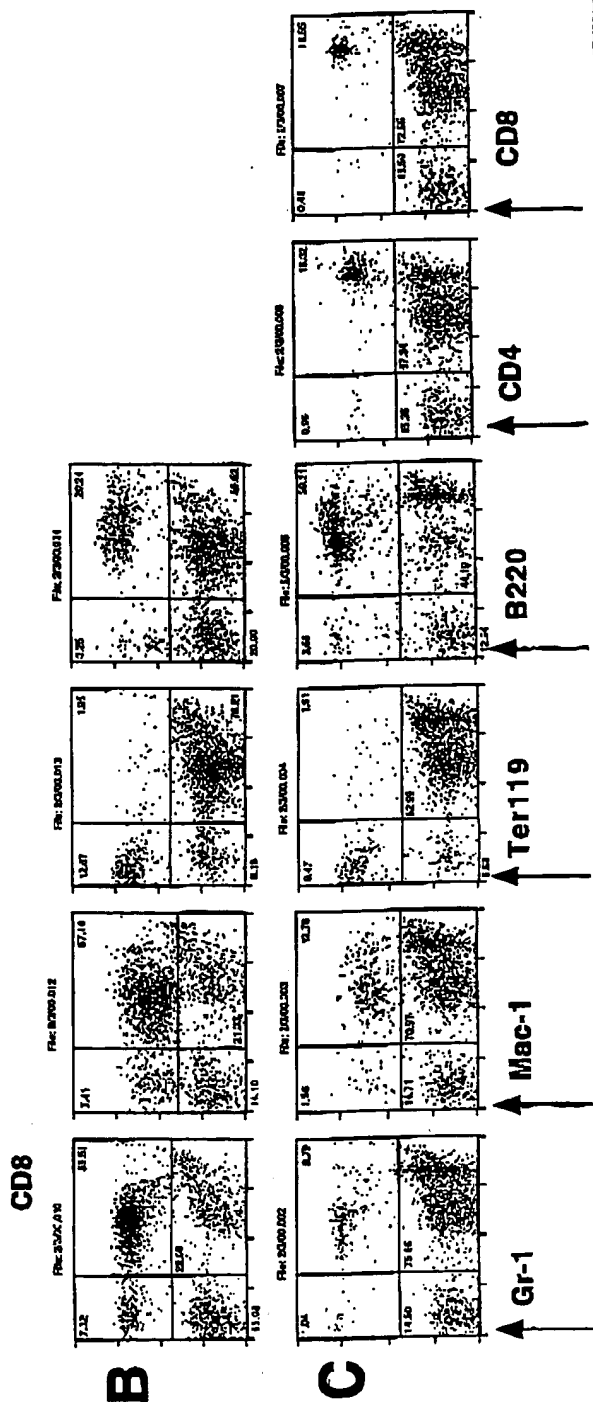
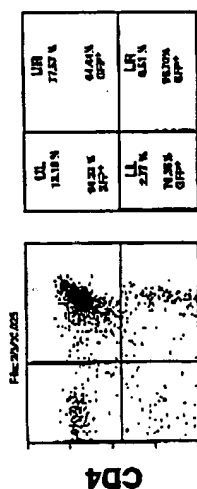
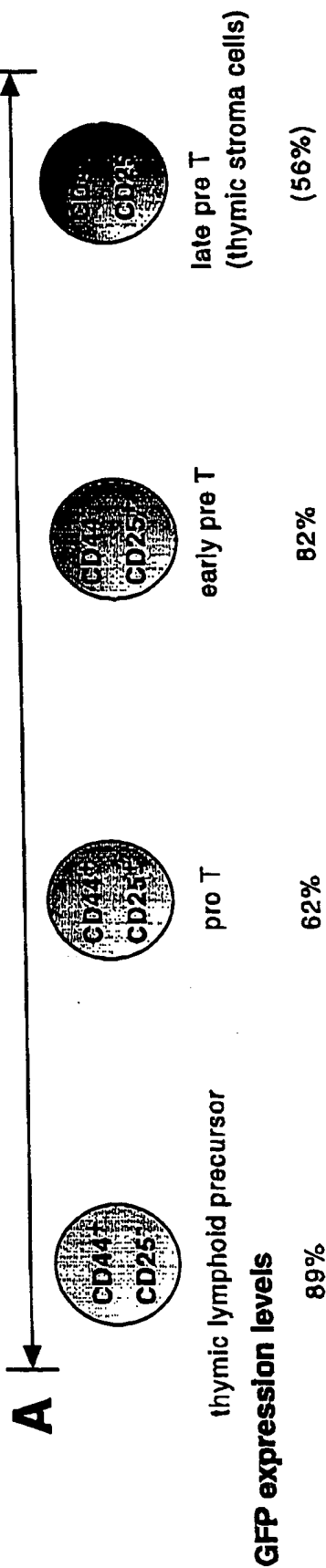


Figure 13